

IN THE SPECIFICATION:

At page 1, after line 2 substitute the following paragraph:

This application is a ~~division~~ divisional of U.S. Serial No. 09/059,461, filed April 14, 1998, ~~allowed~~ now U.S. Patent No. 6,146,894.

At page 19, line 14 to page 20, line 8, substitute the following paragraph:

In vitro translation. Linear DNA fragments containing *hPMS2* and *hMLH1* cDNA sequences were prepared by PCR, incorporating sequences for *in vitro* transcription and translation in the sense primer. A full-length *hMLH1* fragment was prepared using the sense primer 5'-ggatcctaatacgactcactatagggaga ccaccatgtcgttcgtggcaggg-3' (codons 1-6; SEQ ID NO: 3) and the antisense primer 5'-taagtcttaagtgtaccaac-3' (SEQ ID NO: 4; located in the 3' untranslated region, nt 2411-2433), using a wild-type *hMLH1* cDNA clone as template. A full-length *hPMS2* fragment was prepared with the sense primer comprising
~~5'-ggatcctaatacgactcactatagggagaccaccatgatgtttgatcacaatgg-3'~~ 5'- atg gag cga gct gag agc-3' (codons 1- 6; SEQ ID NO: 5) and the antisense primer 5'-aggttagtgaagactctgtc-3' (SEQ ID NO: 6; located in 3' untranslated region, nt 2670-2690) using a cloned *hPMS2* cDNA as template. A fragment encoding the amino-terminal 134 amino acids of *hPMS2* was prepared using the same sense primer and the antisense primer 5'-agtcgagttccaaccttcg-3 (SEQ ID NO: 7). A fragment containing codons 135 - 862 of *hPMS135* was generated using the sense primer 5'-ggatcctaatacgactcactatagggagaccaccatgatgtttgatcacaatgg-3' (SEQ ID NO: 8; codons 135-141) and the same antisense primer as that used for the full-length *hPMS2* protein. These fragments were used to produce proteins via the coupled transcription-translation system (Promega). The reactions were supplemented with ³⁵S-labelled methionine or unlabelled methionine, as indicated in the text. The *PMS135* and *hMLH1* proteins could not be simultaneously radiolabelled and immunoprecipitated because of their similar molecular weights precluded resolution. Lower molecular weight bands are presumed to be degradation products and/or polypeptides translated from alternative internal methionines.

After the claims add the enclosed sequence listing to the application.